GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 1, 2005, 06:51:10 ; Search time 39 Seconds
(without alignments)
24.671 Million cell updates/sec

Title: US-10-780-321-13
Perfect score: 29
Sequence: 1 RXXXRXXXGY 10

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	29	100.0	34	2	F82394	hypothetical prote
2	29	100.0	58	2	S34045	protamine - North
3	29	100.0	60	2	E90041	hypothetical prote
4	29	100.0	62	1	SBHUP	statherin precurso
5	29	100.0	63	2	H72737	probable ribosomal
6	29	100.0	71	2	AG1232	transcription regu
7	29	100.0	77	2	D69010	hypothetical prote
8	29	100.0	77	2	S68955	polyphenolic adhes
9	29	100.0	82	2	S00265	diptericin A - nes
10	29	100.0	88	2	T36233	hypothetical prote
11	29	100.0	89	2	G64381	ribosomal protein
12	29	100.0	92	1	B69041	ribosomal protein
13	29	100.0	94	1	B64331	ribosomal protein
14	29	100.0	94	1	F75022	ribosomal protein
15	29	100.0	95	1	A90257	ribosomal protein
16	29	100.0	99	2	T08060	ribosomal protein
17	29	100.0	99	2	D97652	hypothetical prote
18	29	100.0	101	2	S04634	diptericin D precu
19	29	100.0	101	2	C72467	hypothetical prote
20	29	100.0	102	2	JC1150	hypothetical prote
21	29	100.0	102	2	S21857	hypothetical prote
22	29	100.0	105	2	JC4923	ribosomal protein
23	29	100.0	105	2	A71405	ribosomal protein
24	29	100.0	106	1	R6HU36	ribosomal protein
25	29	100.0	106	1	R6RT36	ribosomal protein
26	29	100.0	106	1	R6UT6A	ribosomal protein
27	29	100.0	106	2	S32481	ribosomal protein
28	29	100.0	106	2	A43301	ribosomal protein
29	29	100.0	106	2	D43301	ribosomal protein
30	29	100.0	107	2	A70943	probable repressor
31	29	100.0	109	1	D71209	ribosomal protein
32	29	100.0	109	2	T40741	very hypothetical
33	29	100.0	112	2	H71041	hypothetical prote
34	29	100.0	120	2	E95343	hypothetical prote
35	29	100.0	121	2	S26798	Ig heavy chain V r
36	29	100.0	125	2	S68170	Ig heavy chain V r
37	29	100.0	125	2	B72517	hypothetical prote
38	29	100.0	128	2	G75308	hypothetical prote
39	29	100.0	129	1	A54119	c-type natriuretic
40	29	100.0	129	2	A85686	probable holin pro
41	29	100.0	132	2	C70161	ribosomal protein
42	29	100.0	132	2	H83048	probable transcrip
43	29	100.0	133	2	S69322	hypothetical prote
44	29	100.0	137	2	I80176	class I histocompa
45	29	100.0	137	2	I38875	MHC class I antige

ALIGNMENTS

RESULT 1
F82394
hypothetical protein VCA0967 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: F82394
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: F82394
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-34 <HEI>
A;Cross-references: UNIPROT:Q9KKY3; GB:AE004423; GB:AE003853; NID:g9658400; PIDN:AAF9686
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0967
A;Map position: 2

Query Match 100.0%; Score 29; DB 2; Length 34;
Best Local Similarity 40.0%; Pred. No. 84;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         21 RMNGRDCHGY 30
```

RESULT 2
S34045
protamine - North American opossum
C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossu
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S34045
R;Winkfein, R.J.; Nishikawa, S.; Connor, W.; Dixon, G.H.
Eur. J. Biochem. 215, 63-72, 1993
A;Title: Characterization of a marsupial sperm protamine gene and its transcripts from t
A;Reference number: S34045; MUID:93345500; PMID:8344286
A;Accession: S34045
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-58 <WIN>
A;Cross-references: UNIPROT:P35305; EMBL:X74044; NID:g407062; PIDN:CAA52193.1; PID:g4070
C;Superfamily: sperm histone
C;Keywords: DNA binding; nucleus

Query Match 100.0%; Score 29; DB 2; Length 58;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         35 RRRGRRGRGY 44
```

RESULT 3
E90041
hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E90041
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E90041
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-60 <KUR>
A;Cross-references: UNIPROT:Q99RM5; GB:BA000018; PID:g13702353; PIDN:BAB43494.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA2192

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  Query Match            100.0%;  Score 29;  DB 2;  Length 60;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         34 RFILRTAIGY 43
```

RESULT 4
SBHUP
statherin precursor [validated] - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: JH0153; A27308; B27489; A03288; A32524
R;Sabatini, L.M.; He, Y.Z.; Azen, E.A.
Gene 89, 245-251, 1990
A;Title: Structure and sequence determination of the gene encoding human salivary stathe
A;Reference number: JH0153; MUID:90323623; PMID:2373369
A;Accession: JH0153
A;Molecule type: DNA
A;Residues: 1-62 <SA2>
A;Cross-references: UNIPROT:P02808; GB:M31077
R;Sabatini, L.M.; Carlock, L.R.; Johnson, G.W.; Azen, E.A.
Am. J. Hum. Genet. 41, 1048-1060, 1987
A;Title: cDNA cloning and chromosomal localization (4q11-13) of a gene for statherin, a
A;Reference number: A27308; MUID:88074310; PMID:3502720
A;Accession: A27308
A;Molecule type: mRNA
A;Residues: 1-62 <SAB>
A;Cross-references: GB:M32639; NID:g338504; PIDN:AAA60593.1; PID:g338506
R;Dickinson, D.P.; Ridall, A.L.; Levine, M.J.
Biochem. Biophys. Res. Commun. 149, 784-790, 1987
A;Title: Human submandibular gland statherin and basic histidine-rich peptide are encode
A;Reference number: A27489; MUID:88106506; PMID:3426601
A;Accession: B27489
A;Molecule type: mRNA
A;Residues: 1-62 <DIC>
A;Cross-references: GB:M18371; NID:g338610; PIDN:AAA60600.1; PID:g338611
R;Schlesinger, D.H.; Hay, D.I.
J. Biol. Chem. 252, 1689-1695, 1977
A;Title: Complete covalent structure of statherin, a tyrosine-rich acidic peptide which
A;Reference number: A03288; MUID:77118656; PMID:838735
A;Accession: A03288
A;Molecule type: protein
A;Residues: 20-62 <SCH>
R;Oppenheim, F.G.; Hay, D.I.; Smith, D.J.; Offner, G.D.; Troxler, R.F.
J. Dent. Res. 66, 462-466, 1987
A;Title: Molecular basis of salivary proline-rich protein and peptide synthesis: cell-fre
gnal peptides.
A;Reference number: A92773; MUID:87309161; PMID:3476566
A;Accession: A32524
A;Molecule type: protein
A;Residues: 1,'X',3-4,'X',6,'X',8,'X',10,'X',12-13,'XX',16 <OPP>
A;Note: radiosequencing of precursor after cell-free translation
C;Comment: Statherin is one of the salivary proteins that stabilize saliva supersaturatec
bly being precursors of enamel pellicle). These inhibitors thus promote enamel stabilizat
C;Genetics:
A;Gene: GDB:STATH
A;Cross-references: GDB:120391; OMIM:184470
A;Map position: 4q11-4q13
A;Introns: 17/3; 24/3; 34/3
C;Superfamily: statherin precursor; statherin/histatin signal sequence homology
C;Keywords: phosphoprotein; saliva
F;1-25/Domain: statherin/histatin signal sequence homology <SHH>
F;1-19/Domain: signal sequence #status experimental <SIG>
F;20-62/Product: statherin #status experimental <MAT>
F;21,22/Binding site: phosphate (Ser) (covalent) #status experimental

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  Query Match            100.0%;  Score 29;  DB 1;  Length 62;
  Best Local Similarity   40.0%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         28 RRIGRFGYGY 37
```

RESULT 5
H72737
probable ribosomal protein L44 APES016 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: H72737
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ku
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyru
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72737
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-63 <KAW>
A;Cross-references: UNIPROT:Q9YF00; DDBJ:AP000059; NID:g5103911; PIDN:BAA79396.1; PID:d1(
A;Experimental source: strain K1
C;Genetics:
A;Gene: APES016
C;Superfamily: rat ribosomal protein L36a

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  Query Match            100.0%;  Score 29;  DB 2;  Length 63;
  Best Local Similarity   40.0%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db          6 RRYRRKQEGY 15
```

RESULT 6
AG1232
transcription regulator homolog lmo1263 [imported] - Listeria monocytogenes (strain EGD-e
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG1232
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1232
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-71 <GLA>
A;Cross-references: UNIPROT:Q8Y7L4; GB:NC_003210; PIDN:CAC99341.1; PID:g16410679; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1263

Query Match 100.0%; Score 29; DB 2; Length 71;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXXRXXXGY 10
|:::|:::||
Db 31 RMGYRYTSGY 40

RESULT 7
D69010
hypothetical protein MTH108 - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69010
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: D69010
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-77 <MTH>
A;Cross-references: UNIPROT:O26211; GB:AE000801; GB:AE000666; NID:g2621145; PIDN:AAB8461
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH108
A;Start codon: TTG

Query Match 100.0%; Score 29; DB 2; Length 77;
Best Local Similarity 40.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXXRXXXGY 10
|:::|:::||
Db 65 RASYRLRVGY 74

RESULT 8
S68955
polyphenolic adhesive protein 3B precursor - Mediterranean mussel
N;Alternate names: foot protein 3B
C;Species: Mytilus galloprovincialis (Mediterranean mussel)
C;Date: 23-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C;Accession: S68955
R;Inoue, K.; Takeuchi, Y.; Miki, D.; Odo, S.; Harayama, S.; Waite, J.H.
Eur. J. Biochem. 239, 172-176, 1996
A;Title: Cloning, sequencing and sites of expression of genes for the hydroxyarginine-cc
A;Reference number: S68954; MUID:96305382; PMID:8706704
A;Accession: S68955
A;Molecule type: mRNA
A;Residues: 1-77 <INO>
A;Cross-references: UNIPROT:Q9GUX7
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-77/Product: polyphenolic adhesive protein 3B #status predicted <MAT>
F;27,28,32,41,44,47,52,55,58,75,77/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #st
F;36,37,46,50,51,63,66,67,72,73/Modified site: 4-hydroxyarginine (Arg) #status predicted

Query Match 100.0%; Score 29; DB 2; Length 77;
Best Local Similarity 40.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXXRXXXGY 10
|:::|:::||
Db 46 RYNGRRYGGY 55

RESULT 9
S00265
diptericin A - nestling-sucking blowfly
C;Species: Protophormia terraenovae (nestling-sucking blowfly)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S00265
R;Dimarcq, J.L.; Keppi, E.; Dunbar, B.; Lambert, J.; Reichhart, J.M.; Hoffmann, D.; Rank
Eur. J. Biochem. 171, 17-22, 1988
A;Title: Insect immunity. Purification and characterization of a family of novel inducib
ence of the predominant member, diptericin A.
A;Reference number: S00265; MUID:88111665; PMID:3276515
A;Accession: S00265
A;Molecule type: protein
A;Residues: 1-82 <DIM>
A;Cross-references: UNIPROT:P10836
C;Keywords: antibacterial

Query Match 100.0%; Score 29; DB 2; Length 82;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXXRXXXGY 10
|:::|:::||
Db 69 RPDYRIGAGY 78

RESULT 10
T36233
hypothetical protein SCE39.23 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36233
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21577
A;Accession: T36233
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-88 <OLI>
A;Cross-references: UNIPROT:Q9X8E6; EMBL:AL049573; PIDN:CAB40331.1; GSPDB:GN00070; SCOED
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCE39.23

Query Match 100.0%; Score 29; DB 2; Length 88;
Best Local Similarity 40.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXXRXXXGY 10
|:::|:::||
Db 21 RVDTRGVSGY 30

RESULT 11
G64381
ribosomal protein L34 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: G64381
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

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A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: G64381
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-89 <BUL>
A;Cross-references: UNIPROT:P54053; GB:U67513; GB:L77117; NID:g1591365; PIDN:AAB98650.1;
C;Genetics:
A;Map position: FOR583166-583435
C;Superfamily: rat ribosomal protein L34

  Query Match             100.0%;  Score 29;  DB 2;  Length 89;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         63 RRPERPYGGY 72


RESULT 12
B69041
ribosomal protein L36a.eR [similarity] - Methanobacterium thermoautotrophicum (strain De
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: B69041
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: B69041
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-92 <MTH>
A;Cross-references: UNIPROT:O27365; GB:AE000895; GB:AE000666; NID:g2622403; PIDN:AAB8578
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1310
C;Superfamily: rat ribosomal protein L36a
C;Keywords: protein biosynthesis; ribosome

  Query Match             100.0%;  Score 29;  DB 1;  Length 92;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         38 RQFRRVTAGY 47


RESULT 13
B64331
ribosomal protein L36a.eR [similarity] - Methanococcus jannaschii
N;Alternate names: ribosomal protein ML44
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: B64331
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: B64331
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-94 <BUL>
A;Cross-references: UNIPROT:P54027; GB:U67480; GB:L77117; NID:g2826265; PIDN:AAB98236.1;
C;Genetics:
A;Map position: FOR235632-235916
C;Superfamily: rat ribosomal protein L36a
C;Keywords: protein biosynthesis; ribosome

  Query Match             100.0%;  Score 29;  DB 1;  Length 94;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         38 RQFRRVTAGY 47


RESULT 14
F75022
ribosomal protein L36a.eR [similarity] - Pyrococcus abyssi (strain Orsay)
N;Alternate names: ribosomal protein l44e PAB1221
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: F75022
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A;Reference number: A75001
A;Accession: F75022
A;Molecule type: DNA
A;Residues: 1-94 <KAW>
A;Cross-references: UNIPROT:Q9UXZ2; GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB5062(
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1221
C;Superfamily: rat ribosomal protein L36a
C;Keywords: protein biosynthesis; ribosome

  Query Match             100.0%;  Score 29;  DB 1;  Length 94;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         38 RRFRRILKGY 47


RESULT 15
A90257
ribosomal protein L36a.eR [similarity] - Sulfolobus solfataricus
N;Alternate names: ribosomal protein L44E
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: A90257
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Y
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: A90257
A;Molecule type: DNA
A;Residues: 1-95 <KUR>
A;Cross-references: UNIPROT:Q97Z81; GB:AE006641; NID:g13814234; PIDN:AAK41312.1; GSPDB:GN
C;Genetics:
A;Gene: rpl44E
C;Superfamily: rat ribosomal protein L36a
C;Keywords: protein biosynthesis; ribosome

  Query Match             100.0%;  Score 29;  DB 1;  Length 95;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         38 RRYERKNIGY 47


Search completed: February  1, 2005, 07:01:30
```

Job time : 41 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 1, 2005, 06:44:50 ; Search time 195 Seconds
(without alignments)
29.506 Million cell updates/sec

Title: US-10-780-321-13
Perfect score: 29
Sequence: 1 RXXXRXXXGY 10

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	29	100.0	34	2	Q9KKY3	Q9kky3 vibrio chol
2	29	100.0	39	2	Q8XRV3	Q8xrv3 ralstonia s
3	29	100.0	43	2	Q8KEJ5	Q8kej5 chlorobium
4	29	100.0	45	2	O18609	O18609 branchiosto
5	29	100.0	48	2	Q9TQC2	Q9tqc2 homo sapien
6	29	100.0	48	2	Q9TQC5	Q9tqc5 homo sapien
7	29	100.0	57	1	HSP1_DIDMA	P35305 didelphis m
8	29	100.0	60	1	HSP1_AEPRU	Q9glp9 aepyprymnus
9	29	100.0	60	2	Q6G6R7	Q6g6r7 staphylococ
10	29	100.0	60	2	Q6GE29	Q6ge29 staphylococ
11	29	100.0	60	2	Q8NV18	Q8nv18 staphylococ
12	29	100.0	60	2	Q99RM5	Q99rm5 staphylococ
13	29	100.0	60	2	Q7A3T4	Q7a3t4 staphylococ
14	29	100.0	60	2	Q9PYU9	Q9pyu9 xestia c-ni
15	29	100.0	61	1	HSP1_TRIVU	P42152 trichosurus
16	29	100.0	62	1	HSP1_SMIGR	Q9tuc3 sminthopsis
17	29	100.0	62	1	STAT_HUMAN	P02808 homo sapien
18	29	100.0	62	2	Q8CJC1	Q8cjc1 rattus norv
19	29	100.0	62	2	AAH67219	Aah67219 homo sapi
20	29	100.0	63	1	HSP1_HYPMS	Q9glq1 hypsiprymno
21	29	100.0	63	1	RL44_AERPE	Q9yf00 aeropyrum p
22	29	100.0	63	2	Q6J1N4	Q6j1n4 burkholderi
23	29	100.0	63	2	Q6Z2B1	Q6z2b1 oryza sativ
24	29	100.0	63	2	BAD01302	Bad01302 oryza sat
25	29	100.0	63	2	BAD01378	Bad01378 oryza sat
26	29	100.0	63	2	AAT38402	Aat38402 burkholde
27	29	100.0	65	2	Q8MHG6	Q8mhg6 pongo pygma
28	29	100.0	65	2	Q8MHG7	Q8mhg7 pongo pygma
29	29	100.0	65	2	Q7UXX1	Q7uxx1 rhodopirell
30	29	100.0	69	2	Q72BC9	Q72bc9 desulfovibr
31	29	100.0	69	2	AAS96184	Aas96184 desulfovi
32	29	100.0	71	2	Q6TLV6	Q6tlv6 macaca fasc
33	29	100.0	71	2	Q8GWM1	Q8gwm1 arabidopsis
34	29	100.0	71	2	Q8Y7L4	Q8y7l4 listeria mo
35	29	100.0	71	2	Q720F9	Q720f9 listeria mo
36	29	100.0	71	2	AAQ95597	Aaq95597 macaca fa
37	29	100.0	71	2	AAT04055	Aat04055 listeria
38	29	100.0	73	2	Q6K3X4	Q6k3x4 oryza sativ
39	29	100.0	74	2	Q86WW8	Q86ww8 homo sapien
40	29	100.0	74	2	Q99M07	Q99m07 mus musculu
41	29	100.0	75	2	Q9J870	Q9j870 spodoptera
42	29	100.0	76	2	Q30203	Q30203 homo sapien
43	29	100.0	76	2	Q8GI72	Q8gi72 salmonella
44	29	100.0	77	2	O26211	O26211 methanobact
45	29	100.0	77	2	Q9GUX7	Q9gux7 mytilus gal

ALIGNMENTS

RESULT 1
Q9KKY3
ID Q9KKY3 PRELIMINARY; PRT; 34 AA.
AC Q9KKY3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein VCA0967.
GN OrderedLocusNames=VCA0967;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AE004423; AAF96863.1; -.
DR PIR; F82394; F82394.
DR TIGR; VCA0967; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 34 AA; 3763 MW; 5CC9711DE0858E56 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 34;
Best Local Similarity 40.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         21 RMNGRDCHGY 30
```

RESULT 2
Q8XRV3
ID Q8XRV3 PRELIMINARY; PRT; 39 AA.
AC Q8XRV3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein RSp0728.
GN Name=RS01700; OrderedLocusNames=RSp0728;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OG Plasmid megaplasmid.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

```
OC   Burkholderiaceae; Ralstonia.
OX   NCBI_TaxID=305;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GMI1000;
RX   MEDLINE=21681879; PubMed=11823852;
RA   Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA   Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA   Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
RA   Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA   Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA   Weissenbach J., Boucher C.A.;
RT   "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL   Nature 415:497-502(2002).
DR   EMBL; AL646080; CAD17879.1; -.
KW   Complete proteome; Hypothetical protein; Plasmid.
SQ   SEQUENCE   39 AA;  4660 MW;  EE5E40DA97913E5E CRC64;

  Query Match            100.0%;  Score 29;  DB 2;  Length 39;
  Best Local Similarity   40.0%;  Pred. No. 4.4e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         24 RQIYRRTVGY 33


RESULT 3
Q8KEJ5
ID   Q8KEJ5      PRELIMINARY;      PRT;    43 AA.
AC   Q8KEJ5;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical protein CT0693.
GN   OrderedLocusNames=CT0693;
OS   Chlorobium tepidum.
OC   Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC   Chlorobaculum.
OX   NCBI_TaxID=1097;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=TLS / ATCC 49652 / DSM 12025;
RX   MEDLINE=22103685; PubMed=12093901; DOI=10.1073/pnas.132181499;
RA   Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA   Dodson R.J., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,
RA   Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F.,
RA   Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,
RA   Parksey D.S., Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B.,
RA   Radune D., Vamathevan J.J., Khouri H.M., White O., Gruber T.M.,
RA   Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT   "The complete genome sequence of Chlorobium tepidum TLS, a
RT   photosynthetic, anaerobic, green-sulfur bacterium.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
DR   EMBL; AE012841; AAM71931.1; -.
DR   TIGR; CT0693; -.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   43 AA;  5354 MW;  EF0A76D438C1C2B7 CRC64;

  Query Match            100.0%;  Score 29;  DB 2;  Length 43;
  Best Local Similarity   40.0%;  Pred. No. 4.9e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db          4 RYFIRRLNGY 13


RESULT 4
O18609
ID   O18609      PRELIMINARY;      PRT;    45 AA.
AC   O18609;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   TR2 (Fragment).
OS   Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
OC   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC   Branchiostoma.
OX   NCBI_TaxID=7740;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97338099; PubMed=9192646;
RA   Escriva H., Safi R., Hanni C., Langlois M.C., Saumitou-Laprade P.,
RA   Stehelin D., Capron A., Pierce R., Laudet V.;
RT   "Ligand binding was acquired during evolution of nuclear receptors.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:6803-6808(1997).
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR   EMBL; U93412; AAB68692.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001628; Znf_C4steroid.
DR   Pfam; PF00105; zf-C4; 1.
DR   SMART; SM00399; ZnF_C4; 1.
KW   DNA-binding; Metal-binding; Nuclear protein; Receptor;
KW   Transcription regulation; Zinc; Zinc-finger.
FT   NON_TER       1      1
FT   NON_TER      45     45
SQ   SEQUENCE   45 AA;  5415 MW;  F509F0B07377F793 CRC64;

  Query Match            100.0%;  Score 29;  DB 2;  Length 45;
  Best Local Similarity   40.0%;  Pred. No. 5.1e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db          6 RRSIRKNLGY 15


RESULT 5
Q9TQC2
ID   Q9TQC2      PRELIMINARY;      PRT;    48 AA.
AC   Q9TQC2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MHC class I HLA-B (Fragment).
GN   Name=HLA-B;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Adams B., McLean I.L., Roberts M., Woodfield D.G.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF011549; AAD46385.2; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00129; MHC_I; 1.
DR   ProDom; PD000050; MHC_I; 1.
FT   NON_TER       1      1
FT   NON_TER      48     48
SQ   SEQUENCE   48 AA;  5841 MW;  DFBEF6652D5B60C3 CRC64;

  Query Match            100.0%;  Score 29;  DB 2;  Length 48;
  Best Local Similarity   40.0%;  Pred. No. 5.4e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         33 RESLRNLRGY 42
```

```
RESULT 6
Q9TQC5
ID   Q9TQC5      PRELIMINARY;      PRT;    48 AA.
AC   Q9TQC5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MHC class I HLA-B (Fragment).
GN   Name=HLA-B;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Adams B., McLean I.L., Roberts M., Woodfield D.G.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF011546; AAD46382.2; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00129; MHC_I; 1.
DR   ProDom; PD000050; MHC_I; 1.
FT   NON_TER       1      1
FT   NON_TER      48     48
SQ   SEQUENCE   48 AA;  5841 MW;  DFBEF6652D5B60C3 CRC64;

  Query Match             100.0%;  Score 29;  DB 2;  Length 48;
  Best Local Similarity   40.0%;  Pred. No. 5.4e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         33 RESLRNLRGY 42


RESULT 7
HSP1_DIDMA
ID   HSP1_DIDMA     STANDARD;      PRT;    57 AA.
AC   P35305;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sperm protamine P1.
GN   Name=PRM1;
OS   Didelphis marsupialis virginiana (North American opossum), and
OS   Monodelphis domestica (Short-tailed grey opossum).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX   NCBI_TaxID=9267, 13616;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=D.marsupialis;
RX   MEDLINE=93345500; PubMed=8344286;
RA   Winkfein R.J., Nishikawa S., Connor W., Dixon G.H.;
RT   "Characterization of a marsupial sperm protamine gene and its
RT   transcripts from the North American opossum (Didelphis marsupialis).";
RL   Eur. J. Biochem. 215:63-72(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.domestica;
RX   MEDLINE=95215351; PubMed=7700877;
RA   Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
RT   "Molecular phylogeny and evolution of marsupial protamine P1 genes.";
RL   Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
CC   -!- FUNCTION: Protamines substitute for histones in the chromatin of
CC       sperm during the haploid phase of spermatogenesis. They compact
CC       sperm DNA into a highly condensed, stable and inactive complex.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- TISSUE SPECIFICITY: Testis.
CC   -!- SIMILARITY: Belongs to the protamine P1 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L17007; AAA02812.1; -.
DR   EMBL; X74044; CAA52193.1; -.
DR   EMBL; L35448; AAA74612.1; -.
DR   PIR; S34045; S34045.
DR   InterPro; IPR000221; Protamine_P1.
DR   Pfam; PF00260; Protamine_P1; 1.
DR   PROSITE; PS00048; PROTAMINE_P1; 1.
KW   Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
KW   Nucleosome core; Spermatogenesis; Testis.
FT   INIT_MET      0      0       By similarity.
SQ   SEQUENCE   57 AA;  7810 MW;  283715B280214E52 CRC64;

  Query Match             100.0%;  Score 29;  DB 1;  Length 57;
  Best Local Similarity   40.0%;  Pred. No. 6.5e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         34 RRRGRRGRGY 43


RESULT 8
HSP1_AEPRU
ID   HSP1_AEPRU     STANDARD;      PRT;    60 AA.
AC   Q9GLP9;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sperm protamine P1.
GN   Name=PRM1;
OS   Aepyprymnus rufescens (Rufous rat-kangaroo) (Rufous bettong).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Diprotodontia; Potoroidae; Aepyprymnus.
OX   NCBI_TaxID=38598;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Burk A., Springer M.S.;
RT   "Intergeneric relationships among Macropodoidea (Metatheria:
RT   Diprotodontia) and the chronicle of kangaroo evolution.";
RL   J. Mammal. Evol. 7:213-237(2000).
CC   -!- FUNCTION: Protamines substitute for histones in the chromatin of
CC       sperm during the haploid phase of spermatogenesis. They compact
CC       sperm DNA into a highly condensed, stable and inactive complex.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- TISSUE SPECIFICITY: Testis.
CC   -!- SIMILARITY: Belongs to the protamine P1 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ---------------------------------------------------------------------
DR   EMBL; AF187547; AAG27964.1; -.
DR   InterPro; IPR000221; Protamine_P1.
DR   PROSITE; PS00048; PROTAMINE_P1; 1.
KW   Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
KW   Nucleosome core; Spermatogenesis; Testis.
FT   INIT_MET      0      0       By similarity.
SQ   SEQUENCE   60 AA;  8445 MW;  1DC24691644A17E0 CRC64;

  Query Match             100.0%;  Score 29;  DB 1;  Length 60;
```

```
  Best Local Similarity   40.0%;  Pred. No. 6.9e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         39 RSRRRRRRGY 48


RESULT 9
Q6G6R7
ID   Q6G6R7      PRELIMINARY;      PRT;    60 AA.
AC   Q6G6R7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Putative membrane protein.
GN   ORFNames=SAS2295;
OS   Staphylococcus aureus subsp. aureus MSSA476.
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=282459;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MSSA476;
RA   Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA   Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA   Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA   Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA   Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA   James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA   Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K., Sanders M.,
RA   Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA   Spratt B.G., Parkhill J.;
RT   "Complete genomes of two clinical Staphylococcus aureus strains:
RT   evidence for the rapid evolution of virulence and drug resistance.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR   EMBL; BX571857; CAG44108.1; -.
SQ   SEQUENCE   60 AA;  6962 MW;  F0136267172B5B22 CRC64;

  Query Match             100.0%;  Score 29;  DB 2;  Length 60;
  Best Local Similarity   40.0%;  Pred. No. 6.9e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         34 RFILRTAIGY 43


RESULT 10
Q6GE29
ID   Q6GE29      PRELIMINARY;      PRT;    60 AA.
AC   Q6GE29;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Putative membrane protein.
GN   ORFNames=SAR2494;
OS   Staphylococcus aureus subsp. aureus MRSA252.
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=282458;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MRSA252;
RA   Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA   Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA   Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA   Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA   Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA   James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA   Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K., Sanders M.,
RA   Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA   Spratt B.G., Parkhill J.;
RT   "Complete genomes of two clinical Staphylococcus aureus strains:
RT   evidence for the rapid evolution of virulence and drug resistance.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR   EMBL; BX571856; CAG41474.1; -.
SQ   SEQUENCE   60 AA;  6931 MW;  6D66A17886A0186B CRC64;

  Query Match             100.0%;  Score 29;  DB 2;  Length 60;
  Best Local Similarity   40.0%;  Pred. No. 6.9e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         34 RFILRTVVGY 43


RESULT 11
Q8NV18
ID   Q8NV18      PRELIMINARY;      PRT;    60 AA.
AC   Q8NV18;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical protein MW2326.
GN   OrderedLocusNames=MW2326;
OS   Staphylococcus aureus (strain MW2).
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=196620;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MW2;
RX   MEDLINE=22040717; PubMed=12044378;
RA   Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA   Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA   Yamamoto K., Hiramatsu K.;
RT   "Genome and virulence determinants of high virulence community-
RT   acquired MRSA.";
RL   Lancet 359:1819-1827(2002).
DR   EMBL; AP004830; BAB96191.1; -.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   60 AA;  6962 MW;  F0136267172B5B22 CRC64;

  Query Match             100.0%;  Score 29;  DB 2;  Length 60;
  Best Local Similarity   40.0%;  Pred. No. 6.9e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         34 RFILRTAIGY 43


RESULT 12
Q99RM5
ID   Q99RM5      PRELIMINARY;      PRT;    60 AA.
AC   Q99RM5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=SAV2404;
OS   Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=158878;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Mu50 / ATCC 700699;
RX   MEDLINE=21311952; PubMed=11418146;
RA   Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA   Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA   Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA   Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA   Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA   Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA   Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT   "Whole genome sequencing of meticillin-resistant Staphylococcus
RT   aureus.";
```

```
RL   Lancet 357:1225-1240(2001).
DR   EMBL; AP003365; BAB58566.1; -.
DR   PIR; E90041; E90041.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   60 AA;  6976 MW;  1CC36267172B5B3A CRC64;

  Query Match             100.0%;  Score 29;  DB 2;  Length 60;
  Best Local Similarity   40.0%;  Pred. No. 6.9e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         34 RFILRTAIGY 43


RESULT 13
Q7A3T4
ID   Q7A3T4      PRELIMINARY;      PRT;    60 AA.
AC   Q7A3T4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein SA2192.
GN   OrderedLocusNames=SA2192;
OS   Staphylococcus aureus (strain N315).
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=158879;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21311952; PubMed=11418146;
RA   Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA   Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA   Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA   Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA   Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA   Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA   Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT   "Whole genome sequencing of meticillin-resistant Staphylococcus
RT   aureus.";
RL   Lancet 357:1225-1240(2001).
DR   EMBL; AP003137; BAB43494.1; -.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   60 AA;  6976 MW;  1CC36267172B5B3A CRC64;

  Query Match             100.0%;  Score 29;  DB 2;  Length 60;
  Best Local Similarity   40.0%;  Pred. No. 6.9e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         34 RFILRTAIGY 43


RESULT 14
Q9PYU9
ID   Q9PYU9      PRELIMINARY;      PRT;    60 AA.
AC   Q9PYU9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ORF94.
GN   Name=ORF94;
OS   Xestia c-nigrum granulosis virus (XnGV) (Xestia c-nigrum
OS   granulovirus).
OC   Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OX   NCBI_TaxID=51677;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99434230; PubMed=10502508;
RA   Hayakawa T., Ko R., Okano K., Seong S.I., Goto C., Maeda S.;
RT   "Sequence analysis of the Xestia c-nigrum granulovirus genome.";
RL   Virology 262:277-297(1999).
DR   EMBL; AF162221; AAF05208.1; -.
SQ   SEQUENCE   60 AA;  7452 MW;  B477BAF7DB2D5930 CRC64;

  Query Match             100.0%;  Score 29;  DB 2;  Length 60;
  Best Local Similarity   40.0%;  Pred. No. 6.9e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         34 RRRSRSRSGY 43


RESULT 15
HSP1_TRIVU
ID   HSP1_TRIVU     STANDARD;      PRT;    61 AA.
AC   P42152;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sperm protamine P1.
GN   Name=PRM1;
OS   Trichosurus vulpecula (Brush-tailed possum).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
OX   NCBI_TaxID=9337;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Sperm;
RX   MEDLINE=95215351; PubMed=7700877;
RA   Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
RT   "Molecular phylogeny and evolution of marsupial protamine P1 genes.";
RL   Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
CC   -!- FUNCTION: Protamines substitute for histones in the chromatin of
CC       sperm during the haploid phase of spermatogenesis. They compact
CC       sperm DNA into a highly condensed, stable and inactive complex.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- TISSUE SPECIFICITY: Testis.
CC   -!- SIMILARITY: Belongs to the protamine P1 family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L32744; AAA99479.1; -.
DR   InterPro; IPR000221; Protamine_P1.
DR   Pfam; PF00260; Protamine_P1; 1.
DR   PROSITE; PS00048; PROTAMINE_P1; 1.
KW   Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
KW   Nucleosome core; Spermatogenesis; Testis.
FT   INIT_MET      0      0       By similarity.
SQ   SEQUENCE   61 AA;  8571 MW;  802287E627EE816C CRC64;

  Query Match             100.0%;  Score 29;  DB 1;  Length 61;
  Best Local Similarity   40.0%;  Pred. No. 7e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db         39 RRRGRRRRGY 48


Search completed: February  1, 2005, 07:00:46
Job time : 198 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 1, 2005, 06:44:50 ; Search time 66 Seconds
(without alignments)
54.353 Million cell updates/sec

Title: US-10-780-321-13
Perfect score: 29
Sequence: 1 RXXXRXXXGY 10

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	29	100.0	10	2	AAR41209	Aar41209 Peptide f
2	29	100.0	10	2	AAR83061	Aar83061 HLA-B7 CT
3	29	100.0	10	2	AAW07518	Aaw07518 T-cell mo
4	29	100.0	10	2	AAW07517	Aaw07517 T-cell mo
5	29	100.0	10	2	AAW07515	Aaw07515 T-cell mo
6	29	100.0	10	2	AAW82806	Aaw82806 Cytomodul
7	29	100.0	10	2	AAW82819	Aaw82819 Cytomodul
8	29	100.0	10	2	AAW82807	Aaw82807 Cytomodul
9	29	100.0	10	2	AAW82809	Aaw82809 Cytomodul
10	29	100.0	10	2	AAW82822	Aaw82822 Cytomodul
11	29	100.0	10	2	AAW82811	Aaw82811 Cytomodul
12	29	100.0	10	2	AAW82816	Aaw82816 Cytomodul
13	29	100.0	10	2	AAW82820	Aaw82820 Cytomodul
14	29	100.0	10	2	AAW82827	Aaw82827 Cytomodul
15	29	100.0	10	2	AAW82821	Aaw82821 Cytomodul
16	29	100.0	10	2	AAW82824	Aaw82824 Cytomodul
17	29	100.0	10	2	AAW82828	Aaw82828 Cytomodul
18	29	100.0	10	2	AAW82804	Aaw82804 Cytomodul
19	29	100.0	10	2	AAW82817	Aaw82817 Cytomodul
20	29	100.0	10	2	AAW82826	Aaw82826 Cytomodul
21	29	100.0	10	2	AAW82829	Aaw82829 Cytomodul
22	29	100.0	10	2	AAW82810	Aaw82810 Cytomodul
23	29	100.0	10	2	AAW82805	Aaw82805 Cytomodul
24	29	100.0	10	2	AAW82813	Aaw82813 Cytomodul
25	29	100.0	10	2	AAW82823	Aaw82823 Cytomodul
26	29	100.0	10	2	AAW82808	Aaw82808 Cytomodul
27	29	100.0	10	2	AAW82814	Aaw82814 Cytomodul
28	29	100.0	10	2	AAW82818	Aaw82818 Cytomodul
29	29	100.0	10	2	AAW82812	Aaw82812 Cytomodul
30	29	100.0	10	2	AAW82815	Aaw82815 Cytomodul
31	29	100.0	10	2	AAW82825	Aaw82825 Cytomodul
32	29	100.0	10	2	AAW33796	Aaw33796 Peptide B
33	29	100.0	10	2	AAW33786	Aaw33786 Peptide B
34	29	100.0	10	4	AAY72486	Aay72486 Immunosup
35	29	100.0	10	4	AAY72485	Aay72485 Immunosup
36	29	100.0	10	4	AAY72496	Aay72496 Immunosup
37	29	100.0	10	4	AAY72494	Aay72494 Immunosup
38	29	100.0	10	4	AAY72487	Aay72487 Immunosup
39	29	100.0	10	4	AAY72497	Aay72497 Immunosup
40	29	100.0	10	4	AAY72495	Aay72495 Immunosup
41	29	100.0	10	4	AAY72493	Aay72493 Immunosup
42	29	100.0	10	6	ABR24478	Abr24478 Human can
43	29	100.0	10	6	ABR25732	Abr25732 Human can
44	29	100.0	10	6	ABR25113	Abr25113 Human can
45	29	100.0	10	6	ABR24876	Abr24876 Human can

ALIGNMENTS

RESULT 1
AAR41209
ID AAR41209 standard; peptide; 10 AA.
XX
AC AAR41209;
XX
DT 25-MAR-2003 (revised)
DT 15-MAR-1994 (first entry)
XX
DE Peptide fragment of Class I HLA peptide.
XX
KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW parasitic disease; cytotoxic T lymphocyte; modulation.
XX
OS Synthetic.
XX
PN WO9317699-A1.
XX
PD 16-SEP-1993.
XX
PF 25-FEB-1993; 93WO-US001758.
XX
PR 02-MAR-1992; 92US-00844716.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
PI Clayberger CA, Krensky AM;
XX
DR WPI; 1993-303134/38.
XX
PT New peptide(s) based on Class I HLA antigen domains - used for modulating
PT cytotoxic T-lymphocyte activity towards targets.
XX
PS Claim 11; Page 54; 61pp; English.
XX
CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity,
CC either by inhibition or stimulation. It can be used for inhibiting CTL
CC toxicity in transplantations, for inducing CTL activity in parasitic
CC diseases and neoplasia and in studies on viral infection. The peptide can
CC also be used for identifying CTLs which bind to it and removing subsets
CC of CTLs from a T-cell composition. This peptide sequence is more commonly
CC found within larger peptide compounds of not more than 30 amino acids in
CC length. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 29; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;

```
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db          1 RESLRNLRGY 10


RESULT 2
AAR83061
ID   AAR83061 standard; peptide; 10 AA.
XX
AC   AAR83061;
XX
DT   15-MAY-1996  (first entry)
XX
DE   HLA-B7 CTL modulating peptide (B7.75-84).
XX
KW   Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW   immunosuppressant; graft versus host disorder; transplantation; therapy;
KW   class I MHC; HLA-B7.
XX
OS   Synthetic.
XX
PN   WO9526979-A1.
XX
PD   12-OCT-1995.
XX
PF   05-APR-1995;   95WO-US004349.
XX
PR   05-APR-1994;   94US-00222851.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Clayberger C,  Krensky AM,  Parham P;
XX
DR   WPI; 1995-358582/46.
XX
PT   Extension of acceptance period of transplants from MHC unmatched donor
PT   hosts - using Class I B75-84 MHC antigen of the recipient host.
XX
PS   Claim 13; Page 66; 80pp; English.
XX
CC   This sequence represents a fragment of a class I major histocompatibility
CC   complex (MHC) antigen. This sequence corresponds to residues 75-84 of the
CC   alpha-1 domain of the class I MHC HLA-B7. This sequence, and the peptide
CC   fragments represented by AAR83062-R83085, AAR83090-R83096 and AAR92907-
CC   R92913 can be used to extend the period of acceptance by a recipient of a
CC   transplant from an MHC unmatched donor. The peptides are administered to
CC   a patient in conjunction with a subtherapeutic amount of an
CC   immunosuppressant. This is administered to the patient for a limited
CC   period of time (compared to the lifetime administration for current
CC   treatments). The peptides particularly modulate (or inhibit) the activity
CC   of the cytotoxic T lymphocytes (CTLs) of the patient
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 29;  DB 2;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db          1 RESLRNLRGY 10


RESULT 3
AAW07518
ID   AAW07518 standard; peptide; 10 AA.
XX
AC   AAW07518;
XX
DT   04-AUG-1997  (first entry)
XX
DE   T-cell modulating peptide #7.
XX
KW   T-cell modulator; autoimmune disease; tissue destruction; alpha1-domain;
KW   mammal; major histocompatability complex; MHC class I; antigen; perforin;
KW   insulin-dependent diabetes mellitus; multiple sclerosis; inflammation;
KW   rheumatoid arthritis; psoriasis; pemphigus vulgaris; Sjogren's disease;
KW   thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme;
KW   autologous target cell; cytokine release; T cell activation; therapy.
XX
OS   Synthetic.
XX
PN   WO9635443-A1.
XX
PD   14-NOV-1996.
XX
PF   05-APR-1996;   96WO-US004710.
XX
PR   12-MAY-1995;   95US-00440504.
XX
PA   (SANG-) SANGSTAT MEDICAL CORP.
XX
PI   Buelow R;
XX
DR   WPI; 1996-518410/51.
XX
PT   Treatment of auto-immune disease by admin. of peptide(s) corresp. to
PT   major histocompatibility complex antigens - esp. for delaying onset of
PT   clinical symptoms of insulin dependent diabetes by modulating T cell
PT   mediated attack on target cells.
XX
PS   Claim 7; Page 20; 24pp; English.
XX
CC   AAW07512-W07518 represent T-cell modulating peptides that can be used in
CC   the method of the invention. These sequences are based on a portion of
CC   the generic peptide corresponding to residues 70-91 of the alpha1-domain
CC   of the major histocompatability complex (MHC) class I antigen (see
CC   AAW07510). The method is for affecting the course of an autoimmune
CC   disease involving T-cell mediated destruction of tissue in mammals. These
CC   peptides are used especially to treat insulin-dependent diabetes
CC   mellitus, preferably being administered during the pre-clinical stage to
CC   delay onset of the disease. Other diseases that can be treated are
CC   multiple sclerosis, rheumatoid arthritis, psoriasis, pemphigus vulgaris,
CC   Sjogren's disease, thyroid disease, Hashimoto's thyroiditis, myasthenia
CC   gravis, etc. The peptides modulate T-cell mediated attack on autologous
CC   target cells, and may also reduce inflammation, swelling, and release of
CC   cytokines, perforins, granzymes etc. associated with T cell activation
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 29;  DB 2;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db          1 RVSLRNLLGY 10


RESULT 4
AAW07517
ID   AAW07517 standard; peptide; 10 AA.
XX
AC   AAW07517;
XX
DT   04-AUG-1997  (first entry)
XX
DE   T-cell modulating peptide #6.
XX
KW   T-cell modulator; autoimmune disease; tissue destruction; alpha1-domain;
KW   mammal; major histocompatability complex; MHC class I; antigen; perforin;
KW   insulin-dependent diabetes mellitus; multiple sclerosis; inflammation;
KW   rheumatoid arthritis; psoriasis; pemphigus vulgaris; Sjogren's disease;
KW   thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme;
```

KW autologous target cell; cytokine release; T cell activation; therapy.
XX
OS Synthetic.
XX
PN WO9635443-A1.
XX
PD 14-NOV-1996.
XX
PF 05-APR-1996; 96WO-US004710.
XX
PR 12-MAY-1995; 95US-00440504.
XX
PA (SANG-) SANGSTAT MEDICAL CORP.
XX
PI Buelow R;
XX
DR WPI; 1996-518410/51.
XX
PT Treatment of auto-immune disease by admin. of peptide(s) corresp. to
PT major histocompatibility complex antigens - esp. for delaying onset of
PT clinical symptoms of insulin dependent diabetes by modulating T cell
PT mediated attack on target cells.
XX
PS Claim 7; Page 20; 24pp; English.
XX
CC AAW07512-W07518 represent T-cell modulating peptides that can be used in
CC the method of the invention. These sequences are based on a portion of
CC the generic peptide corresponding to residues 70-91 of the alpha1-domain
CC of the major histocompatability complex (MHC) class I antigen (see
CC AAW07510). The method is for affecting the course of an autoimmune
CC disease involving T-cell mediated destruction of tissue in mammals. These
CC peptides are used especially to treat insulin-dependent diabetes
CC mellitus, preferably being administered during the pre-clinical stage to
CC delay onset of the disease. Other diseases that can be treated are
CC multiple sclerosis, rheumatoid arthritis, psoriasis, pemphigus vulgaris,
CC Sjogren's disease, thyroid disease, Hashimoto's thyroiditis, myasthenia
CC gravis, etc. The peptides modulate T-cell mediated attack on autologous
CC target cells, and may also reduce inflammation, swelling, and release of
CC cytokines, perforins, granzymes etc. associated with T cell activation
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 29; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXXRXXXGY 10
|:::|:::||
Db 1 RVDLRTLLGY 10

RESULT 5
AAW07515
ID AAW07515 standard; peptide; 10 AA.
XX
AC AAW07515;
XX
DT 04-AUG-1997 (first entry)
XX
DE T-cell modulating peptide #4.
XX
KW T-cell modulator; autoimmune disease; tissue destruction; alpha1-domain;
KW mammal; major histocompatability complex; MHC class I; antigen; perforin;
KW insulin-dependent diabetes mellitus; multiple sclerosis; inflammation;
KW rheumatoid arthritis; psoriasis; pemphigus vulgaris; Sjogren's disease;
KW thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme;
KW autologous target cell; cytokine release; T cell activation; therapy.
XX
OS Synthetic.
XX
PN WO9635443-A1.
XX
PD 14-NOV-1996.
XX
PF 05-APR-1996; 96WO-US004710.
XX
PR 12-MAY-1995; 95US-00440504.
XX
PA (SANG-) SANGSTAT MEDICAL CORP.
XX
PI Buelow R;
XX
DR WPI; 1996-518410/51.
XX
PT Treatment of auto-immune disease by admin. of peptide(s) corresp. to
PT major histocompatibility complex antigens - esp. for delaying onset of
PT clinical symptoms of insulin dependent diabetes by modulating T cell
PT mediated attack on target cells.
XX
PS Claim 7; Page 20; 24pp; English.
XX
CC AAW07512-W07518 represent T-cell modulating peptides that can be used in
CC the method of the invention. These sequences are based on a portion of
CC the generic peptide corresponding to residues 70-91 of the alpha1-domain
CC of the major histocompatability complex (MHC) class I antigen (see
CC AAW07510). The method is for affecting the course of an autoimmune
CC disease involving T-cell mediated destruction of tissue in mammals. These
CC peptides are used especially to treat insulin-dependent diabetes
CC mellitus, preferably being administered during the pre-clinical stage to
CC delay onset of the disease. Other diseases that can be treated are
CC multiple sclerosis, rheumatoid arthritis, psoriasis, pemphigus vulgaris,
CC Sjogren's disease, thyroid disease, Hashimoto's thyroiditis, myasthenia
CC gravis, etc. The peptides modulate T-cell mediated attack on autologous
CC target cells, and may also reduce inflammation, swelling, and release of
CC cytokines, perforins, granzymes etc. associated with T cell activation
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 29; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXXXRXXXGY 10
|:::|:::||
Db 1 RESLRNLRGY 10

RESULT 6
AAW82806
ID AAW82806 standard; peptide; 10 AA.
XX
AC AAW82806;
XX
DT 28-JAN-1999 (first entry)
XX
DE Cytomodulating lipophilic oligopeptide (c).
XX
KW Cytomodulating lipophilic oligopeptide; immune system; inflammation;
KW cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
KW B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
KW Crohn's disease; colitis; allergy; transplant.
XX
OS Synthetic.
XX
PN WO9846633-A1.
XX
PD 22-OCT-1998.
XX
PF 10-APR-1998; 98WO-US007231.
XX
PR 11-APR-1997; 97US-00838916.
PR 23-FEB-1998; 98US-00028083.
XX
PA (SANG-) SANGSTAT MEDICAL CORP.
XX
PI Buelow R, Grassy G, Calas B;

XX
DR WPI; 1998-594558/50.
XX
PT New lipophilic peptide(s) that inhibit activation of immune system cells
PT - used for, e.g. production of cytokine(s) and the inflammatory response,
PT and also for modulating haem-containing enzymes.
XX
PS Claim 7; Page 37; 48pp; English.
XX
CC AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The
CC oligopeptides are used to inhibit: (i) activity of lymphocytes
CC (particularly cytotoxic T cells, but also natural killers, B cells and
CC mononuclear phagocytes); (ii) production of inflammatory cytokines, and
CC (iii) an inflammatory response in mammals (e.g. in cases of septic shock,
CC rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They
CC are also used for modulating activity of haem-containing enzymes and for
CC delaying onset of autoimmune disease (specifically insulin-dependent
CC diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
CC oligopeptides may be generated from nucleic acids, and treatments are in
CC vitro or in vivo. A specific application is treatment of organs or cells
CC for transplantation, or of the recipient of such transplants. Apart from
CC therapeutic use, the oligopeptides can be used to study mechanisms of T
CC cell (de)activation and to raise antibodies (used to identify
CC oligopeptides and to raise anti-idiotypic antibodies that are competitors
CC of the oligopeptides. The oligopeptides are administered by bolus
CC injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
CC Treatment with the oligopeptides increases the life of transplants
XX
SQ Sequence 10 AA;

```
  Query Match             100.0%;  Score 29;  DB 2;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db          1 RILLRLLLGY 10
```

RESULT 7
AAW82819
ID AAW82819 standard; peptide; 10 AA.
XX
AC AAW82819;
XX
DT 28-JAN-1999 (first entry)
XX
DE Cytomodulating lipophilic oligopeptide (p).
XX
KW Cytomodulating lipophilic oligopeptide; immune system; inflammation;
KW cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
KW B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
KW Crohn's disease; colitis; allergy; transplant.
XX
OS Synthetic.
XX
PN WO9846633-A1.
XX
PD 22-OCT-1998.
XX
PF 10-APR-1998; 98WO-US007231.
XX
PR 11-APR-1997; 97US-00838916.
PR 23-FEB-1998; 98US-00028083.
XX
PA (SANG-) SANGSTAT MEDICAL CORP.
XX
PI Buelow R, Grassy G, Calas B;
XX
DR WPI; 1998-594558/50.
XX
PT New lipophilic peptide(s) that inhibit activation of immune system cells
PT - used for, e.g. production of cytokine(s) and the inflammatory response,
PT and also for modulating haem-containing enzymes.
XX
PS Claim 7; Page 37; 48pp; English.
XX
CC AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The
CC oligopeptides are used to inhibit: (i) activity of lymphocytes
CC (particularly cytotoxic T cells, but also natural killers, B cells and
CC mononuclear phagocytes); (ii) production of inflammatory cytokines, and
CC (iii) an inflammatory response in mammals (e.g. in cases of septic shock,
CC rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They
CC are also used for modulating activity of haem-containing enzymes and for
CC delaying onset of autoimmune disease (specifically insulin-dependent
CC diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
CC oligopeptides may be generated from nucleic acids, and treatments are in
CC vitro or in vivo. A specific application is treatment of organs or cells
CC for transplantation, or of the recipient of such transplants. Apart from
CC therapeutic use, the oligopeptides can be used to study mechanisms of T
CC cell (de)activation and to raise antibodies (used to identify
CC oligopeptides and to raise anti-idiotypic antibodies that are competitors
CC of the oligopeptides. The oligopeptides are administered by bolus
CC injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
CC Treatment with the oligopeptides increases the life of transplants
XX
SQ Sequence 10 AA;

```
  Query Match             100.0%;  Score 29;  DB 2;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db          1 RLLWRLLLGY 10
```

RESULT 8
AAW82807
ID AAW82807 standard; peptide; 10 AA.
XX
AC AAW82807;
XX
DT 28-JAN-1999 (first entry)
XX
DE Cytomodulating lipophilic oligopeptide (d).
XX
KW Cytomodulating lipophilic oligopeptide; immune system; inflammation;
KW cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
KW B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
KW Crohn's disease; colitis; allergy; transplant.
XX
OS Synthetic.
XX
PN WO9846633-A1.
XX
PD 22-OCT-1998.
XX
PF 10-APR-1998; 98WO-US007231.
XX
PR 11-APR-1997; 97US-00838916.
PR 23-FEB-1998; 98US-00028083.
XX
PA (SANG-) SANGSTAT MEDICAL CORP.
XX
PI Buelow R, Grassy G, Calas B;
XX
DR WPI; 1998-594558/50.
XX
PT New lipophilic peptide(s) that inhibit activation of immune system cells
PT - used for, e.g. production of cytokine(s) and the inflammatory response,
PT and also for modulating haem-containing enzymes.
XX
PS Claim 7; Page 37; 48pp; English.
XX
CC AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The

```
CC   oligopeptides are used to inhibit: (i) activity of lymphocytes
CC   (particularly cytotoxic T cells, but also natural killers, B cells and
CC   mononuclear phagocytes); (ii) production of inflammatory cytokines, and
CC   (iii) an inflammatory response in mammals (e.g. in cases of septic shock,
CC   rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They
CC   are also used for modulating activity of haem-containing enzymes and for
CC   delaying onset of autoimmune disease (specifically insulin-dependent
CC   diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
CC   oligopeptides may be generated from nucleic acids, and treatments are in
CC   vitro or in vivo. A specific application is treatment of organs or cells
CC   for transplantation, or of the recipient of such transplants. Apart from
CC   therapeutic use, the oligopeptides can be used to study mechanisms of T
CC   cell (de)activation and to raise antibodies (used to identify
CC   oligopeptides and to raise anti-idiotypic antibodies that are competitors
CC   of the oligopeptides. The oligopeptides are administered by bolus
CC   injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
CC   Treatment with the oligopeptides increases the life of transplants
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 29;  DB 2;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db          1 RLVLRLLLGY 10


RESULT 9
AAW82809
ID   AAW82809 standard; peptide; 10 AA.
XX
AC   AAW82809;
XX
DT   28-JAN-1999  (first entry)
XX
DE   Cytomodulating lipophilic oligopeptide (f).
XX
KW   Cytomodulating lipophilic oligopeptide; immune system; inflammation;
KW   cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
KW   B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
KW   Crohn's disease; colitis; allergy; transplant.
XX
OS   Synthetic.
XX
PN   WO9846633-A1.
XX
PD   22-OCT-1998.
XX
PF   10-APR-1998;   98WO-US007231.
XX
PR   11-APR-1997;   97US-00838916.
PR   23-FEB-1998;   98US-00028083.
XX
PA   (SANG-) SANGSTAT MEDICAL CORP.
XX
PI   Buelow R,  Grassy G,  Calas B;
XX
DR   WPI; 1998-594558/50.
XX
PT   New lipophilic peptide(s) that inhibit activation of immune system cells
PT   - used for, e.g. production of cytokine(s) and the inflammatory response,
PT   and also for modulating haem-containing enzymes.
XX
PS   Claim 7; Page 37; 48pp; English.
XX
CC   AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The
CC   oligopeptides are used to inhibit: (i) activity of lymphocytes
CC   (particularly cytotoxic T cells, but also natural killers, B cells and
CC   mononuclear phagocytes); (ii) production of inflammatory cytokines, and
CC   (iii) an inflammatory response in mammals (e.g. in cases of septic shock,
CC   rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They
CC   are also used for modulating activity of haem-containing enzymes and for
CC   delaying onset of autoimmune disease (specifically insulin-dependent
CC   diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
CC   oligopeptides may be generated from nucleic acids, and treatments are in
CC   vitro or in vivo. A specific application is treatment of organs or cells
CC   for transplantation, or of the recipient of such transplants. Apart from
CC   therapeutic use, the oligopeptides can be used to study mechanisms of T
CC   cell (de)activation and to raise antibodies (used to identify
CC   oligopeptides and to raise anti-idiotypic antibodies that are competitors
CC   of the oligopeptides. The oligopeptides are administered by bolus
CC   injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
CC   Treatment with the oligopeptides increases the life of transplants
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 29;  DB 2;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db          1 RLLVRLLLGY 10


RESULT 10
AAW82822
ID   AAW82822 standard; peptide; 10 AA.
XX
AC   AAW82822;
XX
DT   28-JAN-1999  (first entry)
XX
DE   Cytomodulating lipophilic oligopeptide (s).
XX
KW   Cytomodulating lipophilic oligopeptide; immune system; inflammation;
KW   cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
KW   B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
KW   Crohn's disease; colitis; allergy; transplant.
XX
OS   Synthetic.
XX
PN   WO9846633-A1.
XX
PD   22-OCT-1998.
XX
PF   10-APR-1998;   98WO-US007231.
XX
PR   11-APR-1997;   97US-00838916.
PR   23-FEB-1998;   98US-00028083.
XX
PA   (SANG-) SANGSTAT MEDICAL CORP.
XX
PI   Buelow R,  Grassy G,  Calas B;
XX
DR   WPI; 1998-594558/50.
XX
PT   New lipophilic peptide(s) that inhibit activation of immune system cells
PT   - used for, e.g. production of cytokine(s) and the inflammatory response,
PT   and also for modulating haem-containing enzymes.
XX
PS   Claim 7; Page 37; 48pp; English.
XX
CC   AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The
CC   oligopeptides are used to inhibit: (i) activity of lymphocytes
CC   (particularly cytotoxic T cells, but also natural killers, B cells and
CC   mononuclear phagocytes); (ii) production of inflammatory cytokines, and
CC   (iii) an inflammatory response in mammals (e.g. in cases of septic shock,
CC   rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They
CC   are also used for modulating activity of haem-containing enzymes and for
CC   delaying onset of autoimmune disease (specifically insulin-dependent
CC   diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
CC   oligopeptides may be generated from nucleic acids, and treatments are in
CC   vitro or in vivo. A specific application is treatment of organs or cells
```

CC for transplantation, or of the recipient of such transplants. Apart from
CC therapeutic use, the oligopeptides can be used to study mechanisms of T
CC cell (de)activation and to raise antibodies (used to identify
CC oligopeptides and to raise anti-idiotypic antibodies that are competitors
CC of the oligopeptides. The oligopeptides are administered by bolus
CC injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
CC Treatment with the oligopeptides increases the life of transplants
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 29; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db          1 RLLLRLLWGY 10
```

RESULT 11
AAW82811
ID AAW82811 standard; peptide; 10 AA.
XX
AC AAW82811;
XX
DT 28-JAN-1999 (first entry)
XX
DE Cytomodulating lipophilic oligopeptide (h).
XX
KW Cytomodulating lipophilic oligopeptide; immune system; inflammation;
KW cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
KW B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
KW Crohn's disease; colitis; allergy; transplant.
XX
OS Synthetic.
XX
PN WO9846633-A1.
XX
PD 22-OCT-1998.
XX
PF 10-APR-1998; 98WO-US007231.
XX
PR 11-APR-1997; 97US-00838916.
PR 23-FEB-1998; 98US-00028083.
XX
PA (SANG-) SANGSTAT MEDICAL CORP.
XX
PI Buelow R, Grassy G, Calas B;
XX
DR WPI; 1998-594558/50.
XX
PT New lipophilic peptide(s) that inhibit activation of immune system cells
PT - used for, e.g. production of cytokine(s) and the inflammatory response,
PT and also for modulating haem-containing enzymes.
XX
PS Claim 7; Page 37; 48pp; English.
XX
CC AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The
CC oligopeptides are used to inhibit: (i) activity of lymphocytes
CC (particularly cytotoxic T cells, but also natural killers, B cells and
CC mononuclear phagocytes); (ii) production of inflammatory cytokines, and
CC (iii) an inflammatory response in mammals (e.g. in cases of septic shock,
CC rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They
CC are also used for modulating activity of haem-containing enzymes and for
CC delaying onset of autoimmune disease (specifically insulin-dependent
CC diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
CC oligopeptides may be generated from nucleic acids, and treatments are in
CC vitro or in vivo. A specific application is treatment of organs or cells
CC for transplantation, or of the recipient of such transplants. Apart from
CC therapeutic use, the oligopeptides can be used to study mechanisms of T
CC cell (de)activation and to raise antibodies (used to identify
CC oligopeptides and to raise anti-idiotypic antibodies that are competitors
CC of the oligopeptides. The oligopeptides are administered by bolus
CC injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
CC Treatment with the oligopeptides increases the life of transplants
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 29; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db          1 RLLLRVLLGY 10
```

RESULT 12
AAW82816
ID AAW82816 standard; peptide; 10 AA.
XX
AC AAW82816;
XX
DT 28-JAN-1999 (first entry)
XX
DE Cytomodulating lipophilic oligopeptide (m).
XX
KW Cytomodulating lipophilic oligopeptide; immune system; inflammation;
KW cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
KW B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
KW Crohn's disease; colitis; allergy; transplant.
XX
OS Synthetic.
XX
PN WO9846633-A1.
XX
PD 22-OCT-1998.
XX
PF 10-APR-1998; 98WO-US007231.
XX
PR 11-APR-1997; 97US-00838916.
PR 23-FEB-1998; 98US-00028083.
XX
PA (SANG-) SANGSTAT MEDICAL CORP.
XX
PI Buelow R, Grassy G, Calas B;
XX
DR WPI; 1998-594558/50.
XX
PT New lipophilic peptide(s) that inhibit activation of immune system cells
PT - used for, e.g. production of cytokine(s) and the inflammatory response,
PT and also for modulating haem-containing enzymes.
XX
PS Claim 7; Page 37; 48pp; English.
XX
CC AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The
CC oligopeptides are used to inhibit: (i) activity of lymphocytes
CC (particularly cytotoxic T cells, but also natural killers, B cells and
CC mononuclear phagocytes); (ii) production of inflammatory cytokines, and
CC (iii) an inflammatory response in mammals (e.g. in cases of septic shock,
CC rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They
CC are also used for modulating activity of haem-containing enzymes and for
CC delaying onset of autoimmune disease (specifically insulin-dependent
CC diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
CC oligopeptides may be generated from nucleic acids, and treatments are in
CC vitro or in vivo. A specific application is treatment of organs or cells
CC for transplantation, or of the recipient of such transplants. Apart from
CC therapeutic use, the oligopeptides can be used to study mechanisms of T
CC cell (de)activation and to raise antibodies (used to identify
CC oligopeptides and to raise anti-idiotypic antibodies that are competitors
CC of the oligopeptides. The oligopeptides are administered by bolus
CC injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
CC Treatment with the oligopeptides increases the life of transplants
XX
SQ Sequence 10 AA;

```
  Query Match             100.0%;  Score 29;  DB 2;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db          1 RLLLRLLIGY 10


RESULT 13
AAW82820
ID   AAW82820 standard; peptide; 10 AA.
XX
AC   AAW82820;
XX
DT   28-JAN-1999  (first entry)
XX
DE   Cytomodulating lipophilic oligopeptide (q).
XX
KW   Cytomodulating lipophilic oligopeptide; immune system; inflammation;
KW   cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
KW   B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
KW   Crohn's disease; colitis; allergy; transplant.
XX
OS   Synthetic.
XX
PN   WO9846633-A1.
XX
PD   22-OCT-1998.
XX
PF   10-APR-1998;   98WO-US007231.
XX
PR   11-APR-1997;   97US-00838916.
PR   23-FEB-1998;   98US-00028083.
XX
PA   (SANG-) SANGSTAT MEDICAL CORP.
XX
PI   Buelow R,  Grassy G,  Calas B;
XX
DR   WPI; 1998-594558/50.
XX
PT   New lipophilic peptide(s) that inhibit activation of immune system cells
PT   - used for, e.g. production of cytokine(s) and the inflammatory response,
PT   and also for modulating haem-containing enzymes.
XX
PS   Claim 7; Page 37; 48pp; English.
XX
CC   AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The
CC   oligopeptides are used to inhibit: (i) activity of lymphocytes
CC   (particularly cytotoxic T cells, but also natural killers, B cells and
CC   mononuclear phagocytes); (ii) production of inflammatory cytokines, and
CC   (iii) an inflammatory response in mammals (e.g. in cases of septic shock,
CC   rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They
CC   are also used for modulating activity of haem-containing enzymes and for
CC   delaying onset of autoimmune disease (specifically insulin-dependent
CC   diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
CC   oligopeptides may be generated from nucleic acids, and treatments are in
CC   vitro or in vivo. A specific application is treatment of organs or cells
CC   for transplantation, or of the recipient of such transplants. Apart from
CC   therapeutic use, the oligopeptides can be used to study mechanisms of T
CC   cell (de)activation and to raise antibodies (used to identify
CC   oligopeptides and to raise anti-idiotypic antibodies that are competitors
CC   of the oligopeptides. The oligopeptides are administered by bolus
CC   injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
CC   Treatment with the oligopeptides increases the life of transplants
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 29;  DB 2;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db          1 RLLLRWLLGY 10


RESULT 14
AAW82827
ID   AAW82827 standard; peptide; 10 AA.
XX
AC   AAW82827;
XX
DT   28-JAN-1999  (first entry)
XX
DE   Cytomodulating lipophilic oligopeptide (x).
XX
KW   Cytomodulating lipophilic oligopeptide; immune system; inflammation;
KW   cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
KW   B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
KW   Crohn's disease; colitis; allergy; transplant.
XX
OS   Synthetic.
XX
PN   WO9846633-A1.
XX
PD   22-OCT-1998.
XX
PF   10-APR-1998;   98WO-US007231.
XX
PR   11-APR-1997;   97US-00838916.
PR   23-FEB-1998;   98US-00028083.
XX
PA   (SANG-) SANGSTAT MEDICAL CORP.
XX
PI   Buelow R,  Grassy G,  Calas B;
XX
DR   WPI; 1998-594558/50.
XX
PT   New lipophilic peptide(s) that inhibit activation of immune system cells
PT   - used for, e.g. production of cytokine(s) and the inflammatory response,
PT   and also for modulating haem-containing enzymes.
XX
PS   Claim 7; Page 37; 48pp; English.
XX
CC   AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The
CC   oligopeptides are used to inhibit: (i) activity of lymphocytes
CC   (particularly cytotoxic T cells, but also natural killers, B cells and
CC   mononuclear phagocytes); (ii) production of inflammatory cytokines, and
CC   (iii) an inflammatory response in mammals (e.g. in cases of septic shock,
CC   rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They
CC   are also used for modulating activity of haem-containing enzymes and for
CC   delaying onset of autoimmune disease (specifically insulin-dependent
CC   diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
CC   oligopeptides may be generated from nucleic acids, and treatments are in
CC   vitro or in vivo. A specific application is treatment of organs or cells
CC   for transplantation, or of the recipient of such transplants. Apart from
CC   therapeutic use, the oligopeptides can be used to study mechanisms of T
CC   cell (de)activation and to raise antibodies (used to identify
CC   oligopeptides and to raise anti-idiotypic antibodies that are competitors
CC   of the oligopeptides. The oligopeptides are administered by bolus
CC   injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
CC   Treatment with the oligopeptides increases the life of transplants
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 29;  DB 2;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db          1 RLLLRLYLGY 10


RESULT 15
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AAW82821
ID AAW82821 standard; peptide; 10 AA.
XX
AC AAW82821;
XX
DT 28-JAN-1999 (first entry)
XX
DE Cytomodulating lipophilic oligopeptide (r).
XX
KW Cytomodulating lipophilic oligopeptide; immune system; inflammation;
KW cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
KW B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
KW Crohn's disease; colitis; allergy; transplant.
XX
OS Synthetic.
XX
PN WO9846633-A1.
XX
PD 22-OCT-1998.
XX
PF 10-APR-1998; 98WO-US007231.
XX
PR 11-APR-1997; 97US-00838916.
PR 23-FEB-1998; 98US-00028083.
XX
PA (SANG-) SANGSTAT MEDICAL CORP.
XX
PI Buelow R, Grassy G, Calas B;
XX
DR WPI; 1998-594558/50.
XX
PT New lipophilic peptide(s) that inhibit activation of immune system cells
PT - used for, e.g. production of cytokine(s) and the inflammatory response,
PT and also for modulating haem-containing enzymes.
XX
PS Claim 7; Page 37; 48pp; English.
XX
CC AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The
CC oligopeptides are used to inhibit: (i) activity of lymphocytes
CC (particularly cytotoxic T cells, but also natural killers, B cells and
CC mononuclear phagocytes); (ii) production of inflammatory cytokines, and
CC (iii) an inflammatory response in mammals (e.g. in cases of septic shock,
CC rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They
CC are also used for modulating activity of haem-containing enzymes and for
CC delaying onset of autoimmune disease (specifically insulin-dependent
CC diabetes mellitus, RA and systemic lupus erythematosus). In all cases the
CC oligopeptides may be generated from nucleic acids, and treatments are in
CC vitro or in vivo. A specific application is treatment of organs or cells
CC for transplantation, or of the recipient of such transplants. Apart from
CC therapeutic use, the oligopeptides can be used to study mechanisms of T
CC cell (de)activation and to raise antibodies (used to identify
CC oligopeptides and to raise anti-idiotypic antibodies that are competitors
CC of the oligopeptides. The oligopeptides are administered by bolus
CC injection or infusion, typically at 0.1-50 (preferably 1-25) mg/kg.
CC Treatment with the oligopeptides increases the life of transplants
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 29; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 RXXXRXXXGY 10
              |:::|:::||
Db          1 RLLLRLWLGY 10
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Search completed: February 1, 2005, 06:57:23
Job time : 67 secs